SEQUENCE LISTING

<110> Liaw, Gin
Pedersen, Sven
Hendriksen, Sven

<120> A Method of Producing Saccharide Preparations

<130> 5318.200-US

<160> 5

<170> PatentIn version 3.2

<210> 1
<211> 1605
<212> DNA
<213> Aspergillus Niger

<220>
<221> sig_peptide
<222> (1)..(72)

<220>
<221> CDS
<222> (1)..(1602)

<220>
<221> mat_peptide
<222> (73)..(1602)

<400> 1

```
atg tcg ttc cga tct cta ctc gcc ctg agc ggc ctc gtc tgc aca ggg       48
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
                -20                 -15                 -10

ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc       96
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            -5              -1  1               5

aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg      144
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
    10                  15                  20

gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt      192
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
25                  30                  35                  40

ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct      240
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
                45                  50                  55

ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc      288
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
            60                  65                  70
```

```
agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc      336
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
        75                  80                  85

cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc      384
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
    90                  95                  100

ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg      432
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
105                 110                 115                 120

gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc      480
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
                125                 130                 135

ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg      528
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
            140                 145                 150

gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa      576
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
        155                 160                 165

tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg      624
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
    170                 175                 180

tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt      672
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
185                 190                 195                 200

gcc ttc gcg acg gcc gtc ggc tcg tcc tgc tcc tgg tgt gat tct cag      720
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
                205                 210                 215

gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc      768
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
            220                 225                 230

att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc      816
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
        235                 240                 245

ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac      864
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
    250                 255                 260

tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag      912
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
265                 270                 275                 280

gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt      960
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
                285                 290                 295

gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac     1008
```

```
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
            300                 305                 310

aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg     1056
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
        315                 320                 325

tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca     1104
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
    330                 335                 340

gat gtg tcg ctg gac ttc ttc aag gca ctg tac agc gat gct gct act     1152
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
345                 350                 355                 360

ggc acc tac tct tcg tcc agt tcg act tat agt agc att gta gat gcc     1200
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
                365                 370                 375

gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc     1248
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
            380                 385                 390

gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag     1296
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
        395                 400                 405

cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc     1344
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
    410                 415                 420

gcc aac aac cgt cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc     1392
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
425                 430                 435                 440

tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt     1440
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
                445                 450                 455

acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act     1488
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
            460                 465                 470

ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc     1536
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
        475                 480                 485

tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc     1584
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
    490                 495                 500

cgc tct ggt atg tca ctg tga                                        1605
Arg Ser Gly Met Ser Leu
505                 510
```

<210> 2

<211> 534
<212> PRT
<213> Aspergillus Niger

<400> 2

```
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
                -20                 -15                 -10

Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            -5              -1  1               5

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
    10                  15                  20

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
25                  30                  35                  40

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
                45                  50                  55

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
            60                  65                  70

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
        75                  80                  85

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
    90                  95                  100

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
105                 110                 115                 120

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
                125                 130                 135

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
            140                 145                 150

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
        155                 160                 165

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
    170                 175                 180
```

```
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
185                 190                 195                 200

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
                205                 210                 215

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
            220                 225                 230

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
        235                 240                 245

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
    250                 255                 260

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
265                 270                 275                 280

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
                285                 290                 295

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
            300                 305                 310

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
        315                 320                 325

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
    330                 335                 340

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
345                 350                 355                 360

Gly Thr Tyr Ser Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
                365                 370                 375

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
            380                 385                 390

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
        395                 400                 405
```

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
410 415 420

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
425 430 435 440

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
445 450 455

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
460 465 470

Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
475 480 485

Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
490 495 500

Arg Ser Gly Met Ser Leu
505 510

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3
gaatgacttg gttgacgcgt caccagtcac 30

<210> 4
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
ggggatcatg ataggactag ccatattaat gaagggcata taccacgcct tggacctgcg 60

ttatagcc 68

<210> 5
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 5
cctacactgg tccttgggga cggc 24